

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 29, 2003, 18:37:31 ; Search time 1509 Seconds

(without alignments)
333,498 Million cell updates/sec

Title: US-09-750-456-393

Perfect score: 484

Sequence: 1 ccaattcttgcacagagagaga.....gcatatggaactatggtggt 484

Scoring table: IDENTITY: 100%

Gapop 10.0, Gapext 1.0

Searched: 200440 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 410000

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: GenEmbl:*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_cv.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gt_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_cv.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rnd.*
- 36: em_htg_rnd.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	406	93.9	6436	10	PATNIIIA	M96376 Rattus norv
2	366	75.6	5902	9	AB023132	AB023132 Homo sapi
3	366	75.6	6291	9	AB023266	AB023266 Homo sapi
4	270.6	55.9	153169	2	AP001102	AP001102 Homo sapi
5	270.6	55.9	157454	2	AP001462	AP001462 Homo sapi
6	270.6	55.9	164735	2	AC000475	AC000475 Homo sapi
7	270.6	55.9	170114	9	AC004479	AC004479 Homo sapi
8	270.6	55.9	170591	2	AC001139	AC001139 Homo sapi
9	270.6	55.9	203300	9	AC000134	AC000134 Homo sapi
10	200.6	41.4	3044	9	AK000260	AK000260 Homo sapi
11	200.6	41.4	6206	9	AB023255	AB023255 Homo sapi
12	200.6	41.4	8114	9	AB011150	AB011150 Homo sapi
13	198.8	41.1	4149	9	AB013286	AB013286 Homo sapi
14	198.8	41.1	4541	6	AX351021	AX351021 Sequence
15	193.8	40.0	6349	4	BC000000	BC000000 Homo sapi
16	190.8	39.4	7009	10	PATNIIIA	M96374 Rattus norv
17	189	39.0	5609	10	PATNIIIA	M96374 Rattus norv
18	161.8	33.4	4436	5	CGA000473	CGA000473 Gallus ga
19	133.4	27.4	16364	9	AC000745	AC000745 Homo sapi
20	125.2	25.9	73986	2	AC124600	AC124600 Homo sapi
21	124.2	25.7	164427	9	AC000006	AC000006 Homo sapi
22	124	25.6	181217	2	AC101069	AC101069 Mus muscu
23	120.2	24.8	195172	2	AC107855	AC107855 Mus muscu
24	119.6	24.7	161034	2	AC123311	AC123311 Rattus no
25	99	20.5	99072	2	AC130096	AC130096 Rattus no
26	78.6	16.2	179525	2	AC094760	AC094760 Rattus no
27	77.4	16.0	59159	2	AC101311	AC101311 Mus muscu
28	63.2	13.1	106739	2	AC111255	AC111255 Rattus no
29	58.2	12.0	98802	2	AC128547	AC128547 Rattus no
30	50.4	10.4	125020	9	AF429315	AF429315 Homo sapi
31	46	9.5	115666	2	AC105744	AC105744 Oryza sat
32	42.4	8.8	41611	2	AC017806	AC017806 Drosophi
33	42.4	8.8	164193	3	AC006494	AC006494 Drosophi
34	42.4	8.9	179354	3	AC008196	AC008196 Drosophi
35	42.4	8.8	223815	3	AE003739	AE003739 Drosophi
36	42.2	8.7	7219	3	DR000000	M33753 D.melanog
37	42.2	8.7	156905	2	AC020006	AC020006 Drosophi
38	42.2	8.7	199316	3	AC0098204	AC0098204 Drosophi
39	42.2	8.7	204447	3	AE000747	AE000747 Drosophi
40	41.4	8.6	162712	2	AC015677	AC015677 Homo sapi
41	41.4	8.6	164343	9	AP001099	AP001099 Homo sapi
42	41	8.5	157383	2	AC112534	AC112534 Rattus no
43	40.6	8.4	909	1	AB085185	AB085185 Thermus t
44	40.4	8.3	15092	1	AE004204	AE004204 Pseudomon
45	40.4	8.3	15168	1	PSNAPFL	Y15252 Pseudomonas

ALIGNMENTS

RESULT 1	PATNIIIA	6436 bp	mpna	linear	BD 27-APP-1993
LOCUS	PATNIIIA				
DEFINITION	Fallus norvegicus (Rattus norvegicus) Rattus norvegicus (Rattus norvegicus) and minor (alternatively spliced) mRNAs, complete cds.				
ACCESSION	M96376				
VERSION	M96376.1	GI:205714			
KEYWORDS	alpha 1-antitrypsin; cell surface protein; laminin; neurixin II-alpha; synaptic protein.				
SOURCE	Rattus norvegicus (strain Sprague Dawley) (library: Stragene)				
ORGANISM	Rattus norvegicus				
	male brain mRNA				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus				

REFERENCE	1 (bases 1 to 6436)
AUTHOR	Ushikanyev, Y. A., Feltenberg, A. J., Goppert, M. and Sudhof, T. C.
TITLE	Neurexins: synaptic cell surface proteins related to the alpha-lactinin receptor and laminin
JOURNAL	Science 257 (1991), 90-94 (1992)
MEDLINE	92326296
PUBMED	1621994
source	location/qualifiers
	1..6436
	/organism="Rattus norvegicus"
	/strain="Sprague-Dawley"
	/db_xref="taxon:10116"
	/sex="male"
	/tissue_type="brain"
	/tissue_lib="Stratagene"
	join(217..5213,6002..6191)
gene	/gene="neurexin II-alpha"
	join(217..5213,6002..6191)
cds	/gene="neurexin II-alpha"
	/note="minor alternate splicing pattern of neurexins II (less abundant); putative"
	/codon_start=1
	/product="neurexin II-alpha-b"
	/protein_id="AA041706.1"
	/db_xref="GI:205715"
	/translation="MALISFWEFFELPTNLLLAIVAWEGLEFQSSGEMAFYKRWAGASTGELSLFTNATRALILYLDGGMEPLELIVIGLPDLPETISCAEPATIQLDTPVADDRHWMVLLTRDAPRTALAVDGFAPAFVPSKRPQMVASNLFGVGIPIVPLLSALTSTVYVEEFEEFGALATVTEEPFPAVGSGLLETAAGELTAAFNPCATGGICTVLAPGEVGTDSHTGPGKPGKPGKEEHEEMEDPAHLTINSEVSLSESGAGPGGAGNVHQTWAKKEEFVATFQNGSEFYDLSHLLQSTEEITLAFELLENLMHTGVAANYNLSEKGAVMILINGSAFEALVEVNGKFNENAMHGVETNLRCAQIGHAMVNKLHYLVNLSVLGILLTTGYIQEDYTMLSLDEFFYIGSSPTALLPSSPVSNNMGCKPDVYKNDPFRLELSRLKEGDPKMKLQGLSEFQEDVALDPVTESSPEAFVADPRWSAKPTGISLDEPRTENPGLLEFSQGRKAGVGSKSSSQPACVFMELLEGLYLLLDMSGGILTPASSRRKNGGECWCHVDFQPGKPGKISVNSSTPLFADGESEVLDESLEYLGLPEGSHVLLPLPREVMITALRAVVGCVRIFFITGRSRLGLAEAGAVGVAPFSPTETKQVASAPQKRWGIPREMNPFVTDIGTFIIGPVCPEATVLSYFQSMYKMIPLNAMTHEADVSLRPMSQPAGLMMATTSRESADTLPLELDGGMKLTVNLQKLRVGCAPSAAGKETLFGAKHLNENWTLFVPRGKSLQSVENAVEGQWAGAHTELEHNITETIMTEEPFISVGSNFTSLSLVENGQFYMGQCPDQITYCELNAPESLPATVADPVTFRKSPSSYLALATIQAVASMHDFQFKTTAPDGLLFNFGNDPFIIELVFGYTHVYFDLQNSPSIMKNSQKPVNNQWNRVVSPPRGVHTLFINPTVQHSNGARNLLKSELVIGSLSKMNSNLKELVASRQFQGLASVELNGRLDILADALRIGVERGQGGESTTQEESSCANLQVLLWQFTQGLMTSYGQVANNQDTYIFQYGGALITYTPENDLRPSTMDPLAVGESHESAVLVRVDSASLGEVLDLHDGTVGVIFENVSTGCTTIDEFNATVSEKGVHVPRFESQNAATQVGEWPMVEYAGFENEP LAIARQIPYPLQPVDEWLLKGRGLTIFNSQAAKITGPDQGRPMQGVSGLYNG LKVLALAESDPNPVTEGHLPLVGEGPSVLSAETTATTLADMATTIMETTMATT TTRGGSPTMPDSTQNTDQLVASAEQSDDEDEECESPTSGELILPITIEDSLDP PVATRSPPVPPPTFPYFPLTGVGATQDILPPAARPSSSGPGQAEPPDSQCEPVE ASGFASGEVFDSILPPTIDEPFYTLFPLVLTPTTLLSPKPPAPRNLRIDGATGFP LLAPSAPAPNLPAGKMHNPDLQPLLENLPVCPGVTAFRRPPRPPLPGVTSVPGP RLPTANPTGGERGPPGAVEVIRESSITGVVGAALCILILVAYKYPNRCR KSFREELLPQSAQNGGIDILAFACVTPRPATITAGFLLFPFQSSSTETEPIMETIR NK"
mat_peptide	join(298..5213,6002..6198)
	/gene="neurexin II-alpha"
	/product="neurexin II-alpha-b"
	/note="minor alternate splicing pattern of neurexins II (less abundant); putative"
cds	217..5364
	/gene="neurexin II-alpha"
	/note="major splicing pattern of neurexins II (much more abundant)"
	/codon_start=1
	/product="neurexin II-alpha-a"
	/protein_id="AAA41707.1"
	/db_xref="GI:205716"
	/translation="MALGSPWPPEPPQPIILILAIWAGVPIEFQSGPGQAPAYAPWAGAASTGELSLPTNATPAILVITDGGTHTFILLVIGSPIPLPTSCAFPATIQLDTPVADDRHWMVLLTRDAPRTALAVDGEPAAEVPSKRPQMVASDLFGVGIPIVPLLSALTSTVYVEEFEEFGALATVTEEPFPAVGSGLLETAAGELTAAFNPCATGGICTVLAPGEVGTDSHTGPGKPGKPGKEEHEEMEDPAHLTINSEVSLSESGAGPGGAGNVHQTWAKKEEFVATFQNGSEFYDLSHLLQSTEEITLAFELLENLMHTGVAANYNLSEKGAVMILINGSAFEALVEVNGKFNENAMHGVETNLRCAQIGHAMVNKLHYLVNLSVLGILLTTGYIQEDYTMLSLDEFFYIGSSPTALLPSSPVSNNMGCKPDVYKNDPFRLELSRLKEGDPKMKLQGLSEFQEDVALDPVTESSPEAFVADPRWSAKPTGISLDEPRTENPGLLEFSQGRKAGVGSKSSSQPACVFMELLEGLYLLLDMSGGILTPASSRRKNGGECWCHVDFQPGKPGKISVNSSTPLFADGESEVLDESLEYLGLPEGSHVLLPLPREVMITALRAVVGCVRIFFITGRSRLGLAEAGAVGVAPFSPTETKQVASAPQKRWGIPREMNPFVTDIGTFIIGPVCPEATVLSYFQSMYKMIPLNAMTHEADVSLRPMSQPAGLMMATTSRESADTLPLELDGGMKLTVNLQKLRVGCAPSAAGKETLFGAKHLNENWTLFVPRGKSLQSVENAVEGQWAGAHTELEHNITETIMTEEPFISVGSNFTSLSLVENGQFYMGQCPDQITYCELNAPESLPATVADPVTFRKSPSSYLALATIQAVASMHDFQFKTTAPDGLLFNFGNDPFIIELVFGYTHVYFDLQNSPSIMKNSQKPVNNQWNRVVSPPRGVHTLFINPTVQHSNGARNLLKSELVIGSLSKMNSNLKELVASRQFQGLASVELNGRLDILADALRIGVERGQGGESTTQEESSCANLQVLLWQFTQGLMTSYGQVANNQDTYIFQYGGALITYTPENDLRPSTMDPLAVGESHESAVLVRVDSASLGEVLDLHDGTVGVIFENVSTGCTTIDEFNATVSEKGVHVPRFESQNAATQVGEWPMVEYAGFENEP LAIARQIPYPLQPVDEWLLKGRGLTIFNSQAAKITGPDQGRPMQGVSGLYNG LKVLALAESDPNPVTEGHLPLVGEGPSVLSAETTATTLADMATTIMETTMATT TTRGGSPTMPDSTQNTDQLVASAEQSDDEDEECESPTSGELILPITIEDSLDP PVATRSPPVPPPTFPYFPLTGVGATQDILPPAARPSSSGPGQAEPPDSQCEPVE ASGFASGEVFDSILPPTIDEPFYTLFPLVLTPTTLLSPKPPAPRNLRIDGATGFP LLAPSAPAPNLPAGKMHNPDLQPLLENLPVCPGVTAFRRPPRPPLPGVTSVPGP RLPTANPTGGERGPPGAVEVIRESSITGVVGAALCILILVAYKYPNRCR KSFREELLPQSAQNGGIDILAFACVTPRPATITAGFLLFPFQSSSTETEPIMETIR NK"

sig_peptide	/gene="neurexin II-alpha" 297..297 /note="major repeat"
mat_region	/gene="neurexin II-alpha" 298..5361 /note="neurexin II alpha a" /note="major splicing pattern of neurexins II (much more abundant); putative"
repeat_unit	373..1590 /note="major repeat"
repeat_region	/rpt_family="A" /rpt_unit=1156..1590 /rpt_unit=373..771 373..771
repeat_unit	/gene="neurexin II-alpha" /note="neurexin repeat Aa" /rpt_family="A" 832..939 /standard_name="EGF1"
repeat_unit	/rpt_family="EGF" 1156..1590 /gene="neurexin II alpha" /note="neurexin repeat Ab" /rpt_family="A" 1359..1413 /gene="neurexin II-alpha" /note="spliced region" number=1 1518
variation	/gene="neurexin II-alpha" /note="a' in variation" 176..2922
repeat_region	/note="major repeat"
repeat_unit	/rpt_family="B" /rpt_unit=1765..2211 /rpt_unit=2482..2922 1765..2211
repeat_unit	/gene="neurexin II-alpha" /note="neurexin repeat Ba" /rpt_family="B" 2296..2394 /standard_name="EGF2"
repeat_region	/rpt_family="EGF" 2482..2922
repeat_unit	/gene="neurexin II-alpha" /note="neurexin repeat Bb" /rpt_family="B" 2533..2641
misc_feature	

```

/gene="neurexin II-alpha"
/note="spliced region"
/number=2
3043. .4122
/note="major repeat"
/rpt_family="C"
/rpt_unit=3049. .3444
/rpt_unit=3718. .4122
3049. .3444
/gene="neurexin II-alpha"
/note="neurexin repeat Ca"
/rpt_family="C"
3523. .3621
/standard_name="EGF3"
/rpt_family="EGF"
3718. .4122
/gene="neurexin II-alpha"
/note="neurexin repeat Cb"
/rpt_family="C"
3283. .4072
/gene="neurexin II-alpha"
/note="spliced region"
/number=3
4478. .5059
/gene="neurexin II-alpha"
/note="spliced region"
/number=4
5214. .6001
/gene="neurexin II-alpha"
/note="may be spliced out
C-terminal region for cds
2031 c 1978 g 1214 t
to produce alternative
ending at 6191"

```

[illegible]

```

LOCUS       AB023138                5502 bp    mRNA    linear    PRI 10 MAY 2000
DEFINITION  Homo sapiens mPNA for KIA00921 protein, partial cds.
ACCESSION   AB023138
VERSION     AB023138.2  GI:25521693
KEYWORDS
SOURCE      Homo sapiens adult male brain cDNA to mPNA, clone lib.pbluescript
            SK plus clone:ah00573.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1
            Nagase, T., Ishikawa, K., Sugawara, M., Kikuno, R., Hiroseawa, M.,
            Miyajima, N., Tanaka, A., Kettani, H., Nomura, N. and Ohara, O.
            Prediction of the coding sequences of unidentified human genes.
            XIII. The complete sequences of 100 new cDNA clones from brain
            which code for large proteins in vitro
            DNA Res. 6 (1), 63-70 (1999)
JOURNAL     99246063
MEDLINE     10231032
PUBMED
REFERENCE   2  (bases 1 to 5502)
            Ohara, O., Nagase, T. and Kikuno, R.
            Direct Submission
            Submitted (04-FEB-1999) Osamu Ohara, Kazuo DNA Research Institute,
            Laboratory of DNA Technology, Yama 153-2, Yotsukawa, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazuo.or.jp, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
COMMENT     On May 9, 2002 this sequence version replaced gi:4589473.
FEATURES
            Location/Qualifiers
                source

```

[illegible]


```

misc_feature 39444. 52928 /note="assembly_fragment"
misc_feature 51029 62642 /note="assembly_fragment"
misc_feature 62943. 72220 /note="assembly_fragment"
misc_feature 73121 82291 /note="assembly_fragment"
misc_feature 82302. 89905 /note="assembly_fragment"
misc_feature 90096. 97086 /note="assembly_fragment"
misc_feature 97187. 104116 /note="assembly_fragment"
misc_feature 104217. 110763 /note="assembly_fragment"
misc_feature 110864. 116760 /note="assembly_fragment"
misc_feature 116961. 120668 /note="assembly_fragment"
misc_feature 120769. 125393 /note="assembly_fragment"
misc_feature 125494. 128923 /note="assembly_fragment"
misc_feature 129024. 133024 /note="assembly_fragment"
misc_feature 133125. 135479 /note="assembly_fragment"
misc_feature 135580. 138454 /note="assembly_fragment"
misc_feature 138555. 141633 /note="assembly_fragment"
misc_feature 141740. 144205 /note="assembly_fragment"
misc_feature 144306. 147689 /note="assembly_fragment"
misc_feature 147790. 148351 /note="assembly_fragment"
misc_feature 148452. 150846 /note="assembly_fragment"
misc_feature 150947. 152027 /note="assembly_fragment"
misc_feature 152129. 153169 /note="assembly_fragment"
misc_feature 153233. 154273 /note="assembly_fragment"
misc_feature 154374. 155414 /note="assembly_fragment"
misc_feature 155515. 156555 /note="assembly_fragment"
misc_feature 156656. 157696 /note="assembly_fragment"
misc_feature 157797. 158837 /note="assembly_fragment"
misc_feature 158938. 160000 /note="assembly_fragment"
misc_feature 160041. 161204 /note="assembly_fragment"
misc_feature 161307. 162470 /note="assembly_fragment"
misc_feature 162531. 163694 /note="assembly_fragment"
misc_feature 163805. 164968 /note="assembly_fragment"
misc_feature 165141. 166304 /note="assembly_fragment"
misc_feature 166577. 167740 /note="assembly_fragment"
misc_feature 168013. 169176 /note="assembly_fragment"
misc_feature 169609. 170772 /note="assembly_fragment"
misc_feature 171205. 172368 /note="assembly_fragment"
misc_feature 172801. 173964 /note="assembly_fragment"
misc_feature 174397. 175560 /note="assembly_fragment"
misc_feature 175993. 177156 /note="assembly_fragment"
misc_feature 177589. 178752 /note="assembly_fragment"
misc_feature 179185. 180348 /note="assembly_fragment"
misc_feature 180781. 181944 /note="assembly_fragment"
misc_feature 182377. 183540 /note="assembly_fragment"
misc_feature 183973. 185136 /note="assembly_fragment"
misc_feature 185569. 186728 /note="assembly_fragment"
misc_feature 187165. 188317 /note="assembly_fragment"
misc_feature 188761. 190320 /note="assembly_fragment"
misc_feature 190357. 191904 /note="assembly_fragment"
misc_feature 191953. 193500 /note="assembly_fragment"
misc_feature 193549. 195096 /note="assembly_fragment"
misc_feature 195145. 196692 /note="assembly_fragment"
misc_feature 196741. 198288 /note="assembly_fragment"
misc_feature 198337. 199934 /note="assembly_fragment"
misc_feature 199933. 201530 /note="assembly_fragment"
misc_feature 201526. 203123 /note="assembly_fragment"
misc_feature 203119. 204716 /note="assembly_fragment"
misc_feature 204713. 206310 /note="assembly_fragment"
misc_feature 206307. 207904 /note="assembly_fragment"
misc_feature 207897. 209494 /note="assembly_fragment"
misc_feature 209485. 211082 /note="assembly_fragment"
misc_feature 211073. 212660 /note="assembly_fragment"
misc_feature 212657. 214244 /note="assembly_fragment"
misc_feature 214241. 215828 /note="assembly_fragment"
misc_feature 215825. 217412 /note="assembly_fragment"
misc_feature 217411. 218998 /note="assembly_fragment"
misc_feature 218993. 220580 /note="assembly_fragment"
misc_feature 220575. 222156 /note="assembly_fragment"
misc_feature 222147. 223732 /note="assembly_fragment"
misc_feature 223729. 225314 /note="assembly_fragment"
misc_feature 225311. 226896 /note="assembly_fragment"
misc_feature 226887. 228472 /note="assembly_fragment"
misc_feature 228463. 230048 /note="assembly_fragment"
misc_feature 230039. 231624 /note="assembly_fragment"
misc_feature 231625. 233209 /note="assembly_fragment"
misc_feature 233203. 234788 /note="assembly_fragment"
misc_feature 234781. 236366 /note="assembly_fragment"
misc_feature 236359. 237944 /note="assembly_fragment"
misc_feature 237941. 239526 /note="assembly_fragment"
misc_feature 239523. 241104 /note="assembly_fragment"
misc_feature 241101. 242682 /note="assembly_fragment"
misc_feature 242679. 244256 /note="assembly_fragment"
misc_feature 244253. 245830 /note="assembly_fragment"
misc_feature 245827. 247404 /note="assembly_fragment"
misc_feature 247401. 248978 /note="assembly_fragment"
misc_feature 248975. 250552 /note="assembly_fragment"
misc_feature 250549. 252126 /note="assembly_fragment"
misc_feature 252123. 253698 /note="assembly_fragment"
misc_feature 253691. 255264 /note="assembly_fragment"
misc_feature 255257. 256830 /note="assembly_fragment"
misc_feature 256825. 258396 /note="assembly_fragment"
misc_feature 258391. 259962 /note="assembly_fragment"
misc_feature 259957. 261528 /note="assembly_fragment"
misc_feature 261523. 263094 /note="assembly_fragment"
misc_feature 263089. 264660 /note="assembly_fragment"
misc_feature 264655. 266226 /note="assembly_fragment"
misc_feature 266251. 267792 /note="assembly_fragment"
misc_feature 267787. 269358 /note="assembly_fragment"
misc_feature 269353. 270924 /note="assembly_fragment"
misc_feature 270919. 272490 /note="assembly_fragment"
misc_feature 272491. 274056 /note="assembly_fragment"
misc_feature 274053. 275618 /note="assembly_fragment"
misc_feature 275615. 277180 /note="assembly_fragment"
misc_feature 277181. 278742 /note="assembly_fragment"
misc_feature 278737. 280304 /note="assembly_fragment"
misc_feature 280303. 281866 /note="assembly_fragment"
misc_feature 281859. 283428 /note="assembly_fragment"
misc_feature 283425. 284990 /note="assembly_fragment"
misc_feature 284987. 286548 /note="assembly_fragment"
misc_feature 286543. 288106 /note="assembly_fragment"
misc_feature 288101. 289664 /note="assembly_fragment"
misc_feature 289657. 291222 /note="assembly_fragment"
misc_feature 291213. 292780 /note="assembly_fragment"
misc_feature 292779. 294338 /note="assembly_fragment"
misc_feature 294331. 295896 /note="assembly_fragment"
misc_feature 295887. 297454 /note="assembly_fragment"
misc_feature 297451. 299012 /note="assembly_fragment"
misc_feature 299007. 300570 /note="assembly_fragment"
misc_feature 300563. 302128 /note="assembly_fragment"
misc_feature 302119. 303686 /note="assembly_fragment"
misc_feature 303681. 305244 /note="assembly_fragment"
misc_feature 305237. 306802 /note="assembly_fragment"
misc_feature 306793. 308360 /note="assembly_fragment"
misc_feature 308359. 309918 /note="assembly_fragment"
misc_feature 309911. 311476 /note="assembly_fragment"
misc_feature 311467. 313034 /note="assembly_fragment"
misc_feature 313029. 314592 /note="assembly_fragment"
misc_feature 314591. 316150 /note="assembly_fragment"
misc_feature 316147. 317708 /note="assembly_fragment"
misc_feature 317703. 319266 /note="assembly_fragment"
misc_feature 319259. 320824 /note="assembly_fragment"
misc_feature 320821. 322382 /note="assembly_fragment"
misc_feature 322377. 323940 /note="assembly_fragment"
misc_feature 323933. 325498 /note="assembly_fragment"
misc_feature 325489. 327056 /note="assembly_fragment"
misc_feature 327051. 328614 /note="assembly_fragment"
misc_feature 328607. 330172 /note="assembly_fragment"
misc_feature 330171. 331730 /note="assembly_fragment"
misc_feature 331727. 333288 /note="assembly_fragment"
misc_feature 333281. 334846 /note="assembly_fragment"
misc_feature 334837. 336404 /note="assembly_fragment"
misc_feature 336401. 337962 /note="assembly_fragment"
misc_feature 337957. 339520 /note="assembly_fragment"
misc_feature 339513. 341078 /note="assembly_fragment"
misc_feature 341069. 342636 /note="assembly_fragment"
misc_feature 342631. 344194 /note="assembly_fragment"
misc_feature 344187. 345752 /note="assembly_fragment"
misc_feature 345751. 347310 /note="assembly_fragment"
misc_feature 347307. 348868 /note="assembly_fragment"
misc_feature 348861. 350426 /note="assembly_fragment"
misc_feature 350417. 351984 /note="assembly_fragment"
misc_feature 351981. 353542 /note="assembly_fragment"
misc_feature 353537. 355100 /note="assembly_fragment"
misc_feature 355093. 356658 /note="assembly_fragment"
misc_feature 356649. 358216 /note="assembly_fragment"
misc_feature 358211. 359774 /note="assembly_fragment"
misc_feature 359767. 361332 /note="assembly_fragment"
misc_feature 361323. 362890 /note="assembly_fragment"
misc_feature 362887. 364448 /note="assembly_fragment"
misc_feature 364441. 366006 /note="assembly_fragment"
misc_feature 366001. 367564 /note="assembly_fragment"
misc_feature 367557. 369122 /note="assembly_fragment"
misc_feature 369113. 370680 /note="assembly_fragment"
misc_feature 370679. 372238 /note="assembly_fragment"
misc_feature 372231. 373796 /note="assembly_fragment"
misc_feature 373787. 375354 /note="assembly_fragment"
misc_feature 375351. 376912 /note="assembly_fragment"
misc_feature 376907. 378470 /note="assembly_fragment"
misc_feature 378463. 380028 /note="assembly_fragment"
misc_feature 380019. 381586 /note="assembly_fragment"
misc_feature 381581. 383144 /note="assembly_fragment"
misc_feature 3
```

```

Query Match: 55.4%, Size: 176, Length: 1000,
Best Local Similarity: 87.6%, Pred. No. 2, 8e-55;
Matches: 305; Conservative: 0; Mismatches: 41; Indels: 2; Gaps: 2

```

DE 60054 INSTITUTION: ATU; ADDRESS: 1435 N. 103 ST; TULSA, OK 74107

RESULT 5

APR001462/c 157484 bp DNA 1 linear HTG 39 MAY 2000
LEGENS AR001462
REFERENCE: HOMO SAPIENS CHROMOSOME 11 (HOMO SAPIENS CHROMOSOME 11), WORKING
DRAFT SEQUENCE, 33 unordered pieces.

```

ACCESSION   AF001462
VERSION     AF001462.3
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens DNA, clone-PPT-869B15.
ORGANISM    Homo sapiens

```

REFERENCE	1 (bases 1 to 157454)
ACTRESS	Hattori, M., Ishii, Y., Toyoda, A., Taylor, T.D., Hong-Seog, P.

TITLE Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 Homo sapiens 157,454 genomic DNA of 11q13
 JOURNAL Published only in EMBASE (2000)
 REFERENCE 2 (pages 1 to 157454)

<p>AUTHORS</p> <p>Hattori, M., Ishii, K., Toyoda, A., Taylor, T. N., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.</p>	<p>TITLE</p> <p>Direct Submission</p>
<p>REMARK</p> <p>Submitted (15-MAR-2000) Modified (10-APR-2000) Published (10-APR-2000)</p>	<p>Submitted (15-MAR-2000) Modified (10-APR-2000) Published (10-APR-2000)</p>

and Chemical Research (FIFIN), Genomic Sciences Center (GSC), Kitaseito Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail: hattori@gsc.riken.go.jp, npl-hatf./hgp@sc.riken.go.jp, Tel: 81 42 778 9923, Fax: 81 42 778 9924)

RECEIVED
ON MAY 27 1966
U.S. AIR FORCE
OFFICE OF THE
JOINT CHIEFS OF STAFF
WASHINGTON, D.C. 20330-971

----- Genome Center
Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: <http://hpa.go.jp/riken-go.jp/>
Contact: hatornagc@riken.go.jp

----- Project Information -----

Center Project name: HumDrafft1
Center clone name: RP11-869B15

----- Summary Statistics

Sequencing year : 1991-1993, 100% of reads
Chemistry: dye-terminator ET-amersham; 100% of reads

Assembly program: Phxap; version 0.000329

conscious quality. 199493 has at least Q40

Consensus quality: 142529 bases at
Consensus quality: 150042 bases at

Insert size: 154254; sum-of-contents: 154254

[illegible]

NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This result will be dated with the finished sequence as soon as it is available and the accession number will be preserved.

1	20516	contig of	20516	bp in length
20617	30914	contig of	30917	bp in length
42247	53154	contig of	11416	bp in length
63766	73423	contig of	17521	bp in length
73722	81432	contig of	10613	bp in length
84436	88531	contig of	9456	bp in length
93403	93504	contig of	7909	bp in length
94977	98378	contig of	4669	bp in length
101730	106271	contig of	4873	bp in length
106176	110427	contig of	4774	bp in length
114927	114728	contig of	3353	bp in length
114749	114748	contig of	4440	bp in length
122917	120419	contig of	3773	bp in length
			4494	bp in length
			2771	bp in length
			2770	bp in length
			2499	bp in length

```

123018      125127 contig of 2036 bp in length
125209      127891 contig of 2674 bp in length
127982      130914 contig of 2932 bp in length
130915      132593 contig of 1679 bp in length
132594      124516 contig of 1823 bp in length
134617      137106 contig of 2490 bp in length
137207      140498 contig of 3292 bp in length
140599      143489 contig of 2891 bp in length
143590      145559 contig of 1970 bp in length
145660      147741 contig of 2082 bp in length
147842      140318 contig of 1477 bp in length
149419      150896 contig of 1478 bp in length
150997      152442 contig of 1446 bp in length
152543      154192 contig of 1650 bp in length
154293      156330 contig of 2028 bp in length
156431      157454 contig of 1024 bp in length

```

1	20516:	contig of	20516 bp	in length
20517	20616:	gap of	100 bp	
20617	30813:	contig of	10197 bp	in length
30814	30913:	gap of	100 bp	
30914	42329:	contig of	11416 bp	in length
42330	42429:	gap of	100 bp	
42430	53053:	contig of	10624 bp	in length
53054	53153:	gap of	100 bp	
53154	63766:	contig of	10613 bp	in length
63767	63866:	gap of	100 bp	
63867	73322:	contig of	9456 bp	in length
73323	73422:	gap of	100 bp	
73423	81331:	contig of	7909 bp	in length
81332	81431:	gap of	100 bp	
81432	88430:	contig of	6999 bp	in length
88431	88530:	gap of	100 bp	
88531	93403:	contig of	4873 bp	in length
93404	93503:	gap of	100 bp	
93504	98277:	contig of	4774 bp	in length
98278	98377:	gap of	100 bp	
98378	101730:	contig of	3353 bp	in length
101731	101830:	gap of	100 bp	
101831	106170:	contig of	4340 bp	in length
106171	106270:	gap of	100 bp	
106271	110043:	contig of	3773 bp	in length
110044	110143:	gap of	100 bp	
110144	114627:	contig of	4484 bp	in length
114628	114727:	gap of	100 bp	
114729	117498:	contig of	2771 bp	in length
117499	117598:	gap of	100 bp	
117599	120318:	contig of	2720 bp	in length
120319	120418:	gap of	100 bp	
120419	122917:	contig of	2499 bp	in length
122918	123017:	gap of	100 bp	
123018	125107:	contig of	2090 bp	in length
125108	125207:	gap of	100 bp	
125208	127881:	contig of	2674 bp	in length
127882	127981:	gap of	100 bp	
127982	130814:	contig of	2833 bp	in length
130815	130914:	gap of	100 bp	
130915	132593:	contig of	1679 bp	in length
132594	132693:	gap of	100 bp	
132694	134516:	contig of	1823 bp	in length
134517	134616:	gap of	100 bp	
134617	137106:	contig of	2490 bp	in length
137107	137206:	gap of	100 bp	
137207	140498:	contig of	3292 bp	in length
140499	140598:	gap of	100 bp	

*	140593	142480	config of	2891 bp	in length
*	143400	143590	gap of	100 bp	
*	143690	145559	config of	1070 bp	in length
*	145560	145659	gap of	100 bp	
*	145660	147742	config of	2082 bp	in length
*	147742	147841	gap of	100 bp	
*	147842	149318	config of	1477 bp	in length
*	149319	149418	gap of	100 bp	
*	149419	150896	config of	1478 bp	in length
*	150897	150996	gap of	100 bp	
*	150997	152442	config of	1446 bp	in length
*	152443	152542	gap of	100 bp	
*	152543	154192	config of	1650 bp	in length
*	154193	154292	gap of	100 bp	
*	154293	156300	config of	2028 bp	in length
*	156301	156430	gap of	100 bp	
*	156431	157454	config of	1024 bp	in length

FEATURES	Location/Qualifiers
source	1. 157454

```

/misc_feature /organism="Homo sapiens"
/misc_feature /db_xref="taxon:9606"
/misc_feature /chromosome="11"
/misc_feature /map="11q13"
/misc_feature /clone="RP11-869B15"
/misc_feature 1. .20516
/misc_feature /note="assembly_fragment"
/misc_feature 20617. .30813
/misc_feature /note="assembly_fragment"
/misc_feature 30914. .42329
/misc_feature /note="assembly_fragment"
/misc_feature 42430. .53053
/misc_feature /note="assembly_fragment"
/misc_feature 53154. .63766
/misc_feature /note="assembly_fragment"
/misc_feature 63867. .73322
/misc_feature /note="assembly_fragment"
/misc_feature 73422. .81331
/misc_feature /note="assembly_fragment"
/misc_feature 81432. .88430
/misc_feature /note="assembly_fragment"
/misc_feature 88531. .93403
/misc_feature /note="assembly_fragment"
/misc_feature 93504. .98277
/misc_feature /note="assembly_fragment"
/misc_feature 98378. .101730
/misc_feature /note="assembly_fragment clone_end.spc vector_side:right"
/misc_feature 101831 .106170
/misc_feature /note="assembly_fragment"
/misc_feature 106271 .110043
/misc_feature /note="assembly_fragment"
/misc_feature 110144 .114627
/misc_feature /note="assembly_fragment"
/misc_feature 114728 .117498
/misc_feature /note="assembly_fragment"
/misc_feature 117599. .120318
/misc_feature /note="assembly_fragment"
/misc_feature 120419. .122917
/misc_feature /note="assembly_fragment"
/misc_feature 123018 .126107

```

Only Match	55.98%	Score	270.6,	PR	3,	Length	157454,	
Best Local Similarity	87.6%	Pred. No.	2.8e-55,					
Matches 305,	Conservative	0,	Mismatches	42,	Indels	1,	Gaps	1,

2Y	10	000A33A3A3A30GAG3T0CT03AAT0T03A3A3A3T3A30T3TA0T03A30303T0T0T0303A	59
1B	71656	0A0T03A3A3A3003A3ATTT0T3AAT0T3A3A3T3A3TT3TA0T03A30303T0T0T3A	71597
2Y	70	033333AAT3A3T3A3A0CT30TA7T3A7T0T0T3A33T3A33A7A3T0T0T0T0303030G	129
1B	71596	03333330333T3AAT0T3AAT0T3AAT0T3A3A3T3T3A3A3A3T3A3AAT0T03A3T3A3	71537
2Y	130	0TAT0T033T0T0T0T0TA3A3AAT0T0TAT03AT3A3A0T3AT0TANAA3ATTT0T03330G	189

unsure	/product="NRXN2"
unsure	/protein_id="AAK68154.1"
unsure	/db_xref="GI:14573665"
unsure	/translation="MASGSRWPTPPRLDLLLALAAAFADLDEFGGPGQWAFYARWM AGAAAGBELSPSLPTNATPALLVILPDSTQDFLELLLVLPRLPRTLSCAEATLQ LDTPADDPMMHMLTDPDAPRTDLAVDGEAPAAEVRSPREMQASDLFVGQIPDPVR LSALTSTVKKYERPPFRLLANLKLDEEPFALLDSQGLRATAEFLCAPAPNPANGL LTLAPLGEVSLDQSHTGGGKFLDEEHPMEGRPHLLNLSFVSSLSSEKATPQAG DVHQPTGHEEFVATFKQNEFFETLSHNEFGSTTELLAEFTLLQPMGLMHTGSA DYVNLSSKNSJAVMLVINLSSCAFLALVEIVNKKHLNANAEVFTENLSQHASLHAM VNLHLIVTLISVDGLITTSYQDEETLMDSDDEFGFISSEFTNATLPGSIVSNEMSG LKVYVYKNNDEPKLELSRLAKELHEMLLSLSFKCELVALDQVTFEESFEAFALLE WSAKPTQSTLQDPFTTFPQGLLPSQPRAGGAGASHSSAGFADYPAMELNGHLLE LDMSSGGILKLFASSPKVNEGEMIVHVFPRGRKNSLVNSRSTPHLADBSLILLES ELVDGLDESGKRVDLPLFREWMAALPAGVGVGVPRTLETPSPRLPLGLAEAGAVGV APFGSPRTIKQASAPQPNQSVTPQWNPFTDQDTGFLPVPVQPEATVLSYDSMY MKIMLPNAMHTAEADVSLPFGSQAYGLMATTSRESADURLLEDGQMKLTVMIDQ LRVGLAPSKGPEITLFAGKHLNENMHTRVVRGRKSLSLSDVNVTVESQMAAKMKLE FHNIEGTMTDEEPPISSVSPRNPRIQHLQDLVFNQDFVMTQPTGQTYQELNAPRLPA IVALEVTFKRSSTYLALATLQAYASMHLPQPYRTAPDQLPFGNGNPRTVETVPI GYHYVFDLGNHSLMKNSKFEVNNQNMHNVSPDEANHTLKHDSNTVSHSNQAA ENLDRJELLYLQSLSKMSENLKFLVASGRGFGGLASVLLNQLLELLALALHEIQ VEEJLJESTLTFEESQAMLVGLLQWSEGTQVMSVSLVQVQDSTYIEKQDM LITYTWPNDRPSTPMDPLAVSGSTHQPASVLVEVSSASQIDYLLHLHFGTAVIE NVGTDQTLIDEENALVSGQGHVAVRTTSGGNATLVQSMVNHYPAPJNEHEFLAIL APQPIPYPLTPVDEWLLKRGQNTFNSQAAIKTGRPTTFPFGQVSGLYNGIKV LALAESDPNVRTGHLRLVSGEGSVLLSAETTATULLAMATTIMETTTMATPTTP RPSFTLPNSTTQNTQNLVASAEPSPDEDELEETEPSTGSLILPITTFQSLNPPPV ATPSPEVPPRPTEFYPPLTGVQATQVQDILLIPYAPAPPSQATPQAEPLDSEDEEPIEASG FASGEVPESSLPDDEDFDTTFLPVTDPRTULSPKRPAPPNRPTGATGAPGVLPFA PSAPAKRLAAGLMHREFLQLEHFLPBAFTSEELPHTFLFVTSAPQFENHLL TANPTGGERGPPGAVEVIRESSITGMVVGIVAAALDILLILLYAMYKVRNDEGSY QVDCSRNYSNACSNJAVVEKAVAAHETFEAAKHHNLEHYV"
unsure	11700. 11840
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	15980. 15986
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	16030. 16036
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	23225. 23252
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	26059. 26066
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	26212. 26239
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	74307. 74326
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	74456. 74468
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	74549. 74591
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	74816. 74828
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	74969. 74997
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	76872. 77010
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	77101. 77110
unsure	/gene="NRXN2"
unsure	/note="low quality data"
unsure	80775. 80780

```

/ gene="NRXN2"
/ note="low quality data"
106199 106400
/ gene="NRXN2"
/ note="low quality data"
110547..1170114
/ note="overlap with RPS 1045021, AC012153"
110547..1170114
complete(join(116447..116510,117060..117263,
117622..117631,118108..118322,119075..119199,
119359..119482,124195..124363,124430..124593,
125117..125219,126043..126441))
/ note="44 clones (146548-146551) from cDNA library; exon boundaries defined in relation to mouse cDNA AB05451"
/codon_start=1
/product="RST"
/protein_id="AAK68156.1"
/db_xref="GI:14573667"
/translation="MAFSEELVWVGLFVVDQMALMVGIMWDSGMLEFSAVY
PSHFWARLLDNRSTQASISLSEPAIATIPPPNPEFHRRHQWMLDPN
ATATMSSEADDEPVTGWVYVGRILSTIAVWNLVLSHATFMAISILVGA
AAVPSSEFSEELVWISILQKAMSTAAFAFEIVQDFLAFVAVGMNTGT
TLEMENTAAPRLVMLNELSEFBSHDAVAVSWITLLVSVFFLEGLYS
WMAESAPMLITFSLCWQSLWVVAALNKGAVLSTLEVLVAVFHTSMQDP
ASLQTLPMPTGFPTTISTCWPAFGFTFSLALDQALGSLFLQMFVGVDIRA
FMALILSHRDFEFTLAAQLLALCILATTCVHEKACRQALATVQLGVGAFT

```


LOCUS	AC000134.1	203300 bp	ENA	linear	FRI 06 MAY 1999
DEFINITION	Human sapiens Chr. 7: 11q13 FAF 21000-110000, 11q13 sapiens				
ACCESSION	AC000134				
VERSION	AC000134.14	GI:4755212			
KEYWORDS	HTG				
SOURCE	Homio sapiens.				
ORGANISM	Homio sapiens				
	Eukaryotic, Metazoa, Chordata, Mammalia, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.				
REFERENCE	1 (bases 1 to 203300)				
AUTHORS	Crabtree, J., and Roe, B.A.				
TITLE	Sequence of a 11q13 bac mapping to PYGM				
JOURNAL	Unpublished (1997)				
REFERENCE	2 (bases 1 to 203300)				
AUTHORS	Chandrasekharappa, S.G., Guru, S.G., Manickam, P., Gilefisi, S.-E. and Collins, F.S.				
TITLE	Sequence of a 11q13 bac mapping to PYGM				
JOURNAL	Unpublished (1997)				
REFERENCE	3 (bases 1 to 203300)				
AUTHORS	Fewerl-Ruck, M.P., Debelenko, I.V., Zhuang, Z., Lubensky, I.A. and Liotta, L.A.				
TITLE	Sequence of a 11q13 bac mapping to PYGM				
JOURNAL	Unpublished (1997)				
REFERENCE	4 (bases 1 to 203300)				
AUTHORS	Weismann, J. and Boguski, M.S.				
TITLE	Sequence of a 11q13 bac mapping to PYGM				
JOURNAL	Unpublished (1997)				
REFERENCE	5 (bases 1 to 203300)				
AUTHORS	Ajizawa, S.K., Foster, M., Kim, Y.-J., Heffer, J., F. 103/2, Spiegel, A.M., Burns, L.A. and Marx, S.J.				
TITLE	Sequence of a 11q13 bac mapping to PYGM				
JOURNAL	Unpublished (1997)				
REFERENCE	6 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-MAR-1997) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	7 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-APR-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	8 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-APR-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	9 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-MAY-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	10 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-MAY-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	11 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-MAY-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	12 (bases 1 to 203300)				
AUTHORS	Roe, B.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-MAY-1999) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Farrington Oval, Room 208, Norman, OK 73019, USA				
REFERENCE	12 (bases 1 to 203300)				

[illegible]


```

DEFINITION Homo sapiens mPNA for KIAA0743 protein, complete cds.
ACCESSION AB018286
AB018286.1 GI:3982206
KEYWORDS
SOURCE Homo sapiens adult male brain cDNA to mRNA, clone lib.FJ058911
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria, Primates; Catarrhini; Hominoidea, HOMO.
AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,F., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
JOURNAL DNA Res. 5 (5), 277-286 (1998)
MEDLINE 99087487
REFERENCE 2 (bases 1 to 4149)
AUTHORS Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,F.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1998) Genome Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 242-0292, Japan E-mail: ohara@fuk.kazusa.or.jp, Tel:+81 438 52-2073, Fax:+81-438-52-3914)
FEATURES
Source
location=1..4149
organism="Homo sapiens"
db_xref="taxon:9606"
clone="hk04080"
sex="male"
tissue_type="brain"
clone_id="PBuescriptII SK plus"
dev_stage="adult"
1..4149
/gene="KIAA0743"
492..3677
/gene="KIAA0743"
/codon_start=1
/product="KIAA0743 protein"
/protein_id="BAA34463.1"
/db_xref="GI:3982207"
translation="MLGSDDFPVYVGGSPSTADLPGSPVSNFMGLKEVVYKKNDIPLELSRLARIADTKMKLYGEVEFKENQENATLDPINFETPEAYISLPKNTRKMSISPDPGRTEPNGLILFTHGKPPQEPKPAPSQNTRKVDPAVELIDGNLYILIMSGSTIKVKATQRYANGEMWYHTTTFEDPSSTISVNSRTEFFIASSEELLEGMYLGSIFENFAGLILPLEMTAMLVGVVCIRLEFIIGRSKNIQLAEHQNAAGVKSQSPMAKQITSSYPCKNNAVCKDGMRFICDCTGTGYWGRTCEERASILSYDSGMVMKIIMPVWHTEAEADVSRFMSQRAYGLIVATTSRSDADTLRIELDGSPVKUMVNIDCIRINSSGKPPETTVAQOKLNQNEHWTPVPVPGSKLKLTVDQDAEGTWGDHPLEPHNTFTGITMPKVYISVPPSFIGHLOSIMFNGLVIDICKNGDIYCELFPAGFLNIIADPTFTPSGVYLSLATQAITYSMLEPFQFTSPDGFIENSQDNDEIAYELVGYYHYVEFLQNPRNVIKMREEFLENEMHWVTTPINSSTHETKVFQVTVTGANTFEISGLATAETAQMGYSNLKLVASRPTFGSLASVCLNHLPELLINDALHRSAQIKQTDEPSTQOEDESCANGVCMQMEGFCDCSMTSYSNQNDPSATYIEKSGGLIAYTMFAHREESTRSDPLAVGSTFTVDTGLVIPIDAPSGIDDELQHIEGHFGVENFTGVIDISTFREPTPVNDKYHVHVRFTFNDGNATLLQVDNMFVNEHYPRFULTENTGAQIALGKRRRIEAFQQLSLGLYEGLKLVNMAAENNPNIKINGSVELVGPVSLGITQTTSMRPESSTVWEETTMATTTRKRPTASIQFTSDPLVSAGESSLETTFVECEFTASTATEPPIFEVPGASEVIRESSSTIGMWVGIVAAALCILILLYAMVYKYPNDEGSYQVDETENYISNSAQSNGTLMKEKQSSKSHKKQKNKLREYV"
BASE COUNT 1073 A 1063 C 1076 G 937 T
ORIGIN
Query Match 41.1%; Score 158.8, E=9, Length 4149,
Best Local Similarity 66.0%; Pred No 8 3e-38;
Matches 311; Conservative 0; Mismatches 156; Indels 4; Gaps 27

```

[illegible][illegible]

LOCUS 6149 bp mRNA linear MAR 09 AUG 1995
DEFINITION Bos taurus neurexin I alpha mRNA, complete cds
ACCESSION U14855
VERSION U14855.1 GI:388560
KEYWORDS neurexin I-alpha.
SOURCE Bos taurus taurin
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bos.
REFERENCE 1 (bases 1 to 6349)
AUTHORS Gillich, B., Ushkaryov, Y.A. and Sukhof, T.C.
TITLE Cartography of neurexins: more than 1000 isoforms generated by
alternative splicing and expressed in distinct subsets of neurons
JOURNAL Neuron 14 (3), 497-507 (1995)
MEDLINE 95209856
PUBMED 7695896

FEATURES
source
location/Qualifiers
1..6349
/organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="brain"
1293..5885
/note="amino acid information: bases 1381 5657
extracellular domain; amino acid information: bases 5355
5567 O-glycosylation domain; amino acid information:
bases 5658 5717 transmembrane domain; amino acid
information: bases 5718 5980 cytoplasmic domain;
precursor"
/codon_start=1
/product="neurexin I-alpha"
/protein_id="AAA74123.1"
/db_xref="GI:388561"

CDs
LOCUS 6149 bp mRNA linear MAR 09 AUG 1995
DEFINITION Bos taurus neurexin I alpha mRNA, complete cds
ACCESSION U14855
VERSION U14855.1 GI:388560
KEYWORDS neurexin I-alpha.
SOURCE Bos taurus taurin
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bos.
REFERENCE 1 (bases 1 to 6349)
AUTHORS Gillich, B., Ushkaryov, Y.A. and Sukhof, T.C.
TITLE Cartography of neurexins: more than 1000 isoforms generated by
alternative splicing and expressed in distinct subsets of neurons
JOURNAL Neuron 14 (3), 497-507 (1995)
MEDLINE 95209856
PUBMED 7695896

18021 JVENV3111AIEENALIN3KH7TFE333ATTCVTCWYIERPA
GNDNERLAIAPQIPYPIGVYDEMILTPQPLIENSAI1116FFED3GFOQL
SGYTRGLVILMAENDANAVGNVLVGEVPSWTESTATAMGSEWTSIMETT
TTLATSTAPKPKPTKEPVSQTDILIVASABCPDDEIDPCPSSGGLANPTRAG
KEPIFSAHVIKESSSTIMVGVIAAAALDILIDAMVYRNEDEDS3HYDERSNY
ISNSAGSNARVFRPCPSAKKANNRKRDEYV"
1293..1382
/evidence=experimental
mat_peptide
1383..5882
/product="neurexin I-alpha"
/function="presynaptic cell surface protein"
/evidence=experimental
1457..2699
/note="major repeat A; putative"
/rpt_family="neurexin repeat"
1452..1865
/note="left arm Aa of the major repeat A; putative"
/rpt_family="neurexin repeat"
1941..2057
/note="EGF repeat 1, epidermal growth factor; putative"
/rpt_family="EGF"
2065..2172
/note="spliceable sequence, splice site 1"
/evidence=experimental
2262..2699
/note="right arm Ab of the major repeat A; putative"
/rpt_family="neurexin repeat"
2475..2519
/note="spliceable sequence, splice site 2"
/evidence=experimental
2871..4019
/note="major repeat B; putative"
/rpt_family="neurexin repeat"
2871..3314
/note="left arm Ba of the major repeat B; putative"
/rpt_family="neurexin repeat"
3375..3497
/note="EGF repeat 2; epidermal growth factor; putative"
/rpt_family="EGF"
3513..4019
/note="right arm Bb of the major repeat B; putative"
/rpt_family="neurexin repeat"
3709..3735
/note="spliceable sequence, splice site 3"
/evidence=experimental
4146..5225
/note="major repeat C; putative"
/rpt_family="neurexin repeat"
4146..4541
/note="left arm Ca of the major repeat C; putative"
/rpt_family="neurexin repeat"
4599..4718
/note="EGF repeat 3, epidermal growth factor; putative"
/rpt_family="EGF"
4815..5225
/note="right arm Cb of the major repeat C; putative"
/rpt_family="neurexin repeat"
5080..5169
/note="spliceable sequence, splice site 4"
/evidence=experimental
5569..5577
/note="spliceable sequence, splice site 5"
/evidence=experimental
5690
/note="a' in variation"
/replace=""

BASE COUNT 1680 a 1598 c 1660 g 1411 t
ORIGIN
Query Match 40 98 Score 199.9; DB 4; Length 6349;
Best Local Similarity 66 28; Pred. No. 132-361;
Matches 109; Mismatches 161; Indels 4; Gaps 2;

[illegible]

```

Search completed. March 29, 2003, 22:37:42
Job time : 1982 secs

```

•

•

•